

PT	Nucleic acid encoding gibberellin inhibitor GAI and related			
PT	antisense sequences - used to create tall, or particularly, dwarf			
PT	plants, especially crops such as maize, rice and wheat			
XX	Claim 1; Fig 4; 76pp; English.			
PS				
XX	The present sequence is the Arabidopsis thaliana gibberellin			
CC	insensitivity (gai) gene product (GAI), the expression of which			
CC	inhibits plant growth. However the inhibition is antagonised by			
CC	gibberellin (GA), while gai expression confers a dwarf phenotype			
CC	that is insensitive to GA. Manipulating gai and GAI expression can			
CC	produce tall or dwarf plants, particularly the latter for increased			
CC	resistance to lodging and increased yield. It may also allow			
CC	regulation of flowering, i.e. plants remain in the vegetative state			
CC	until treated with GA, useful to inhibit bolting in spinach and			
CC	lettuce. GAI can be used to raise specific antibodies for			
CC	identifying homologous proteins or genes in other species. gai			
CC	fragments can also be used as probes or primers to identify and			
CC	clone related sequences, or in the preparation of antisense or			
CC	sense expression regulating (co-suppressing) sequences. Rice plants			
CC	that express GAI may be resistant to Bakane disease. Manipulation			
CC	of gai and GAI makes it possible to tailor the degree of dwarfism			
CC	and GA sensitivity to particular crops or situations.			
XX				
SQ	Sequence 532 AA;			
Query Match 100.0%; Score 2758; DB 18; Length 532;				
Best Local Similarity 100.0%; Pred. No. 1.5e-256;				
Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
QY	1	MKRDRHHHQDKTKMMNEEDGNGMDLLAVLGKVKRSSEMDVAQKLEQLEVMNSVQ	60	
DB	1	mkrdrhhhhqdktkmmneeedgngmdllavlgvkvrssmadvaqkleglevmnsnvq	60	
QY	61	EDDISOLATEVHYNPAELYTWDSMLTDLNPPSSNAEYDLKAIPGDAILNQFAIDSASS	120	
DB	61	eddisqlatetvhympaeltytwdsmltdlnppssnaeydikaipgdailnqfaidsass	120	
QY	121	SNQGGGGDTYTNKRKLCNSGVVETTTATAESTRHVLVDSQENGVRVLHALLACAEAVQ	180	
DB	121	snqggggdtytnkrkcsngvvetttataestrhvvlvdsqengvrvlhallacaeavq	180	
QY	181	KENLTVAEALVKQIGFLAVSOGAMRKVATYFAELARRIYRLSPSQPIDHSLDITLQM	240	
DB	181	kenltvaealvkqigflavsqigamrkvatyfaealarriyrlspsqspidhsidsitlqm	240	
QY	241	HFYETCPYLKFAHTANQAIIEAFQKKRVHVIDFMSOGLQWPALMOALALRPGGPPVF	300	
DB	241	hfyetcpylkfahfanaqaiieafqgkkrvividfmsqglqwpalmqalalrpggppvf	300	
QY	301	RLTGIGPPAPDNFDYLHEVGCKLAHAEAIHVEFEYRGFVANTLADLDASMLELRPSEIE	360	
DB	301	rltligppapdnfdylhevvgcklahlaeahivefeyrgfvanltladldasmlerlseie	360	
QY	361	SVAVNSVFELHLLGRPCAIDKVLGVVNIQIKPEITFTVVEQESNHSNPFIDRFETSLHYI	420	
DB	361	svavnsvfelhlgrpcaidkvlgvvniqikpeiftftvvegesnhsnplfdrfetslhyi	420	
QY	421	STLFDLSLGEVSGQDKVNSEYVLGKICNVVACDGPDRVERHETLSQWRNRFSGAGFAA	480	
DB	421	stlfdslgevspgqdkvnmseyylgkicnvvacdgpdrverhetlsqwrnrfsgagfaa	480	
QY	481	HIGSNAFKQASMLIALFNGGEGYRVESDGCIMLGWHTRPRIATSAWKLSN 532		
DB	481	higsnafkqasmllalfnggegryrveesdgcimlgwhtprlriatsawklstn 532		
RESULT 2				
AAE02545				
ID	AAE02545 standard; Protein: 532 AA.			
XX				
AC	AAE02545;			

XX	10-AUG-2001	(first entry)	
DT	A. thaliana transcription factor G308.		
XX	Plant transcription factor; phenotype; sugar sensing characteristic;		
XX	transgenic plant; plant yield; growth; germination; photosynthesis;		
KW	glyoxylate metabolism; respiration; pathogen response; wounding response;		
KW	cell cycle regulation; pigmentation; flowering; senescence; physiology;		
KW	storage organ; metabolism.		
OS	Arabidopsis thaliana.		
XX			
XX	Key	Location/Qualifiers	
FT	Domain	270..274	
FT	/note= "Conserved domain"		
XX	WO200135725-A1.		
PN	25-MAY-2001.		
PD	14-NOV-2000; 2000WO-US31414.		
XX	17-NOV-1999; 99US-0166228.		
PR	17-APR-2000; 2000US-0197899.		
PR	22-AUG-2000; 2000US-0227439.		
XX	(MEND-) MENDEL BIOTECHNOLOGY INC.		
PA	(JIAN/) JIANG C.		
PA	(HEAR/) HEARD J.		
PA	(PINE/) PINEDA O.		
PA	(PILG/) PILGRIM M.		
PA	(ADAM/) ADAM L.		
PA	(RIEC/) RIECHMANN J L.		
PA	(YUGG/) YU G.		
PA	(SAMA/) SAMAHA R.		
XX	Jiang C, Heard J, Pineda O, Pilgrim M, Adam L, Riechmann JL;		
PI	Yu G, Samaha R;		
XX	WPI: 2001-335977/35.		
DR	N-PSDB: AAD06646.		
XX	Nucleic acids encoding plant transcription factor polypeptides, useful		
PT	for altering the sugar sensing characteristics of plants and increasing		
PPT	yield, e.g. corn, potato and cotton plants -		
PPT	Claim 4; Page 74-76; 151pp; English.		
XX	The patent relates to polynucleotides encoding 35 plant transcription		
CC	factors which may be used to modify phenotype associated with a plant's		
CC	sugar sensing characteristics and increasing yield when their expression		
CC	level is altered. Sugars are central regulatory molecules that control		
CC	aspects of physiology, metabolism and development. Therefore the cDNAs		
CC	and proteins of the invention are useful for modifying the growth and		
CC	germination rates of plants, photosynthesis, glyoxylate metabolism,		
CC	respiration, starch and sucrose synthesis and degradation, pathogen		
CC	response, wounding response, cell cycle regulation, pigmentation,		
CC	flowering and senescence of plants and for modifying sink-source		
CC	relationships in seeds, tubers, roots, and other storage organs leading		
CC	to an increase in yield. The transcription factor polynucleotides and		
CC	polypeptides may be used to alter the structure and developmental		
CC	characteristics of plants such as soybean, wheat, corn, potato, cotton,		
CC	rice, oilseed, sunflower, alfalfa, sugarcane, turf, banana, blackberry,		
CC	blueberry, strawberry, raspberry, cantaloupe, carrot, cauliflower,		
CC	coffee, cucumber, eggplant, grapes, honey dew, lettuce, mango, melon,		
CC	onion, papaya, peas, peppers, pineapple, spinach, squash, sweet corn,		
CC	tobacco, tomato, watermelon, rosaceous fruits and/or vegetable brassicas.		
CC	The present sequence is an Arabidopsis thaliana transcription factor.		
XX	Sequence 532 AA;		
SQ			

Query Match 99.9%; Score 2754; DB 22; Length 532;
Best Local Similarity 99.8%; Pred. No. 3.7e-256;
Matches 531; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKRDHHHHQDKKTMNMNEEDGNGMDLLAVLGYKVRSEMDVYKQLEQLEVMMSNVQ 60
DB 1 mkrdhhhhqdkktnmneeedgngmdllavlgvkvrssemadvakleqlevmmsnvq 60

QY 61 EDDLSQLATETVHYNPAELYTWLDSMLTDLNPPSSNAEYDKAIPGDAILNQFAIDSASS 120
DB 61 eddlsqlatetvhynpaelytwldsmldtnppssnaeydkaipgdailnqfaidsass 120

QY 121 SNQGGGGDTYTNKRLKCSNGVVTATTAESTRHVVLVDSQENGVRVHALLACAEAVQ 180
DB 121 snqggggdtytnkrlkcsngvvttataestrhvvldsqengvrivhallacaeavq 180

QY 181 KENLTVAEALVKQIGFLAVSQIGAMRKVATYFAEALARRIYRLSPSQSPIDHSLSDTLQM 240
DB 181 kenltvaealvkqigflavsqigamrqvatyfaealarriryrlspsqspidhslsdtlqm 240

QY 241 HFYETCPYLKFAHFTANQALILEAFQKKRVHVVDIFSMSGLOWPALMQALALRPGGPPVF 300
DB 241 hfetcpylkfahftanqaileafqgkkrvhvvdifsmgsglqwpalmqalalrpggppvf 300

QY 301 RLTGIGPPAPDNFDYLVHEVGCKLAHLAEAIHVEFEYRGFVANTLADLDSMLELRPSEIE 360
DB 301 rltgigppapdnfdylvhevgcklahlaeahivefeyrgfvantladldasmlelrpseie 360

QY 361 SVAVNSVFELHKLGRPGAIDKVLGVNQIKPEITVVQESNHNPSPIFLDRFTESLHY 420
DB 361 svavnsvfelhklgrpgaidkvlgvnmqikpeitvvqesnhnpspifldrfteslhy 420

QY 421 STLFDSLEGVPSGQDKVMSEVYLGKQICNVACDGPDRVERHETLSQWNRFGSAGFAAA 480
DB 421 stlfdslgvpvgqdkvmsevylgkicnvvacdgpdrverhetlsqwnrfgsagfaaa 480

QY 481 HIGSNFAKQASMLLALFNGGEGYRVEESDGLMLGWHTRPLIATSAWKLSN 532
DB 481 higsnafkasmlalflnggegryveesdglmlgwhtrpliatsawklstn 532

RESULT 3
AAE01907
ID AAE01907 standard; Protein; 532 AA.
XX
AC AAE01907;
DT
DT 31-JUL-2001 (first entry)
XX
DE Arabidopsis thaliana transcription factor, G308.
XX
KW Transcription factor; biochemical characteristic; controlling element;
KW structural characteristic; developmental characteristic; gene therapy;
KW agricultural biotechnology; plant trait modification.
XX
OS Arabidopsis thaliana.
XX
FH Key Location/Qualifiers
FT Domain 270..274
FT /label= Conserved_domain
XX
PN WO200136597-A1.
XX
PD 25-MAY-2001.
XX
XX 14-NOV-2000; 2000WO-US31344.
XX
PR 17-NOV-1999; 99US-0166228.
PR 17-APR-2000; 2000US-0197899.
PR 22-AUG-2000; 2000US-0227439.
XX
PA (MEND-) MENDEL BIOTECHNOLOGY INC.
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PA (HEAR/) HEARD J.
PA (SAMA/) SAMAH R.
PA (PILG/) PILGRIM M.
PA (PINE/) PINEDA O.
PA (JIAN/) JIANG C.
XX
XX Creelman R, Yu G, Adam L, Riechmann JL, Heard J, Samaha R;
PI Pilgrim M, Pineda O, Jiang C;
XX
XX WPI: 2001-335999/35.
XX N-PSDB: AAD05791.
XX
XX Nucleic acids encoding plant transcription factor polypeptides, useful
PT for altering the biochemical characteristics of plants e.g. corn,
PT potato and cotton plants -
XX
XX Claim 4; Page 114-115; 127pp; English.
XX
XX The present sequence is Arabidopsis thaliana transcription factor,
CC G308, a homologue of G307. The transcription factor is used for altering
CC a plant's biochemical characteristics. The transcription factor may be
CC used to alter the structure and developmental characteristics of plants
CC such as soybean, wheat, corn, potato, cotton, rice, oilseed rape,
CC sunflower, alfalfa, sugar cane, turf, banana, blackberry, blueberry,
CC strawberry, raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber,
CC eggplant, grapes, honey dew, lettuce, mango, melon, onion, papaya, peas,
CC peppers, pineapple, spinach, squash, sweet corn, tobacco, tomato,
CC watermelon, roseaceous fruits and/or vegetable brassicas. Transcription
CC factors are key controlling elements of biological pathways and altering
CC expression levels of 1 or more transcription factors can change entire
CC biological pathways in an organism. Therefore manipulating transcription
CC factor levels in plants offers great potential in agricultural
CC biotechnology for modifying a plant's traits. Transcription factor cDNA
CC is useful in gene therapy.
XX
XX Sequence 532 AA;
SQ

Query Match 99.9%; Score 2754; DB 22; Length 532;
Best Local Similarity 99.8%; Pred. No. 3.7e-256;
Matches 531; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKRDHHHHQDKKTMNMNEEDGNGMDLLAVLGYKVRSEMDVYKQLEQLEVMMSNVQ 60
DB 1 mkrdhhhhqdkktnmneeedgngmdllavlgvkvrssemadvakleqlevmmsnvq 60

QY 61 EDDLSQLATETVHYNPAELYTWLDSMLTDLNPPSSNAEYDKAIPGDAILNQFAIDSASS 120
DB 61 eddlsqlatetvhynpaelytwldsmldtnppssnaeydkaipgdailnqfaidsass 120

QY 121 SNQGGGGDTYTNKRLKCSNGVVTATTAESTRHVVLVDSQENGVRVHALLACAEAVQ 180
DB 121 snqggggdtytnkrlkcsngvvttataestrhvvldsqengvrivhallacaeavq 180

QY 181 KENLTVAEALVKQIGFLAVSQIGAMRKVATYFAEALARRIYRLSPSQSPIDHSLSDTLQM 240
DB 181 kenltvaealvkqigflavsqigamrqvatyfaealarriryrlspsqspidhslsdtlqm 240

QY 241 HFYETCPYLKFAHFTANQALILEAFQKKRVHVVDIFSMSGLOWPALMQALALRPGGPPVF 300
DB 241 hfetcpylkfahftanqaileafqgkkrvhvvdifsmgsglqwpalmqalalrpggppvf 300

QY 301 RLTGIGPPAPDNFDYLVHEVGCKLAHLAEAIHVEFEYRGFVANTLADLDSMLELRPSEIE 360
DB 301 rltgigppapdnfdylvhevgcklahlaeahivefeyrgfvantladldasmlelrpseie 360

QY 361 SVAVNSVFELHKLGRPGAIDKVLGVNQIKPEITVVQESNHNPSPIFLDRFTESLHY 420
DB 361 svavnsvfelhklgrpgaidkvlgvnmqikpeitvvqesnhnpspifldrfteslhy 420

Qy 421 STLFDSLEGVSPGQKVMSEVYLGKQICNVVACDGPDRVERHETLSQWRNREGSAGFAAA 480
Db 421 stlfdslgvpqgdkvmsevylgkqicnvvacdgpdrverhetlsqwrnrfgsagfaaa 480
Qy 481 HIGSNAPKQASMLIALFNGGEGYRVEESDGLMLGWHTRPRIATSAWKLSTN 532
Db 481 higsnafkqasmlialfnggegryveesdgclmigmwhtprliatsawklstn 532

RESULT 4
AAG38575
ID AAG38575 standard; Protein: 533 AA.
XX
AC AAG38575;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 47610.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.

CC SCARECROW-like (SCL) genes encoding proteins containing an amino acid
CC sequence similar to the sequence of MOTIF III (VHID) of Arabidopsis SCR
CC protein are disclosed. SCR and SCL genes are useful for producing
CC transgenic plants whose cell division is modified and root and/or stem
CC development and gravitropism of stem or hypocotyl is altered. Cell
CC division is increased or decreased in roots resulting in thicker or
CC thinner root development. The transgenic plants are useful for expressing
CC a gene of interest encoding a gene product that confers herbicide, salt,
CC pathogen or insect resistance in root or embryos and genes encoding
CC starch, lignin or cellulose biosynthesis in shoots. The SCR gene also
CC confers less susceptibility to lodging in the transgenic plants than a
CC wild-type plant. SCR gene sequences are also useful as molecular markers
CC for a quantitative trait e.g. root or gravitropism trait in molecular
CC breeding of crop plants.

XX Sequence 531 AA;

Query Match 99.3%; Score 2739.5; DB 21; Length 531;
Best Local Similarity 99.6%; Pred. No. 9.1e-255;
Matches 530; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
Oy 1 MKRDHHHHQDKKTKMMNEEDGNGMDLLAVLGKVRSSMADVAOKLEOVMMNNVQ 60
Db 1 mkrdhhhhqdkktkmmneeddngmdellavlgkvrssmadvaokleovmnnvq 60
Oy 61 EDDLSQLATETVHYNPAELYTWLDSMLTDLNPPSSNAEYDLKIPGDAILNQFAIDSASS 120
Db 61 eddlsqlatetvhynpaelytwldsmldtnppssnaeydlkaipgd-ilnqfaidsass 119
Oy 121 SNQGGGGTYTNNKRLKCSNGVWTTTATAESTRHVVLVDSQGVRLVHALLACAEAVQ 180
Db 120 snqgggggtyttnkrkcsngvvtattataestrhvvldsgengvrlvhallacaeavq 179
Oy 181 KENITVAELVKQIGFLAVSIOIGAMRKVATYFAEALARRIYRLSPSOPIDHSLSDTLQM 240
Db 180 kenitvaealvkqigflavsigamrkvatyfaealarriryrlspssopidhsldtlqm 239
Oy 241 HFYETCPYLKFAHTANQAILEAFQGGKRVHVDFSMSSQGLQWPAALALRPGGPPVF 300
Db 240 hfyetcpylkfahntanqaileafqgkkrvhvdfmsqglqwpalmaqalalrpggppvf 299
Oy 301 RLITGGPPAPDNFDYHEVGCKLAHLARAIHVEFEYGFVANTLADLDASMLELRPSFIE 360
Db 300 rlitgppapdnfdyhevvgcklhlaeahihvefeygfvantladldasmlerpsfiele 359
Oy 361 SVAVNSVPELHKLGRPGAIDKVLGVNQNQIKPEIFTVVEQSNHNSPIFLDRFTESLHY 420
Db 360 svavnsvfelhkllgrpgaikdvlgvnnqikpeiftvveqesnhnspifldrfteslhy 419
Oy 421 STLFDSEGVSPGQDKVMSEVYLGKICNVVACDGPDRVERHETLSQWNRNRFSGAGFAA 480
Db 420 stlfdsegvspgqdkvmsevylgkicnvvacdgpdrverhetlsqwnrfsgagfaa 479
Oy 481 HIGSNAFKQASMLALFNGGEGYVESDGLMLGHWTRPLIATSAWKLSTN 532
Db 480 higsnafkqasmallfnggegryveesdgcmlmgwtrpliatkawklstn 531

RESULT 6

AAG38576
ID AAG38576 standard; Protein; 518 AA.
AC AAG38576;
XX
XX
DT 18-OCT-2000 (first entry)
DE Arabidopsis thaliana protein fragment SEQ ID NO: 47611.

XX Protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.

OS Arabidopsis thaliana.
XX EPI033405-A2.
PN
XX
XX
PD 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-0301439.
PF 99US-0121825.
PR 99US-0123180.
PR 99US-0123548.
PR 99US-0125788.
PR 99US-0126284.
PR 99US-0126785.
PR 99US-0127462.
PR 99US-0128234.
PR 99US-0128714.
PR 99US-0129845.
PR 99US-0130077.
PR 99US-0130449.
PR 99US-0130510.
PR 99US-0130891.
PR 99US-0131449.
PR 99US-0132048.
PR 99US-0132407.
PR 99US-0132484.
PR 99US-0132485.
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PR 99US-0134218.
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PR 99US-0134221.
PR 99US-0134370.
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PR 99US-0134941.
PR 99US-0135124.
PR 99US-0135353.
PR 99US-0135629.
PR 99US-0136021.
PR 99US-0136392.
PR 99US-0136782.
PR 99US-0137222.
PR 99US-0137528.
PR 99US-0137502.
PR 99US-0137724.
PR 99US-0138094.
PR 99US-0138540.
PR 99US-0138847.
PR 99US-0139119.
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PR 99US-0139458.
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PR 99US-0139461.
PR 99US-0139462.
PR 99US-0139463.
PR 99US-0139750.
PR 99US-0139763.
PR 99US-0139817.
PR 99US-0139899.
PR 99US-0140353.
PR 99US-0140354.
PR 99US-0140695.
PR 99US-0140823.
PR 99US-0140991.

PR	30-JUN-1999;	99US-0141287.
PR	01-JUL-1999;	99US-0141842.
PR	01-JUL-1999;	99US-0142154.
PR	02-JUL-1999;	99US-0142055.
PR	06-JUL-1999;	99US-0142390.
PR	08-JUL-1999;	99US-0142803.
PR	09-JUL-1999;	99US-0142920.
PR	12-JUL-1999;	99US-0142977.
PR	13-JUL-1999;	99US-0143542.
PR	14-JUL-1999;	99US-0143624.
PR	15-JUL-1999;	99US-0144005.
PR	16-JUL-1999;	99US-0144085.
PR	16-JUL-1999;	99US-0144086.
PR	19-JUL-1999;	99US-0144325.
PR	19-JUL-1999;	99US-0144331.
PR	19-JUL-1999;	99US-0144332.
PR	19-JUL-1999;	99US-0144333.
PR	19-JUL-1999;	99US-0144334.
PR	20-JUL-1999;	99US-0144335.
PR	20-JUL-1999;	99US-0144352.
PR	20-JUL-1999;	99US-0144632.
PR	20-JUL-1999;	99US-0144884.
PR	21-JUL-1999;	99US-0144814.
PR	21-JUL-1999;	99US-0145086.
PR	21-JUL-1999;	99US-0145088.
PR	22-JUL-1999;	99US-0145085.
PR	22-JUL-1999;	99US-0145087.
PR	22-JUL-1999;	99US-0145089.
PR	22-JUL-1999;	99US-0145192.
PR	23-JUL-1999;	99US-0145145.
PR	23-JUL-1999;	99US-0145218.
PR	23-JUL-1999;	99US-0145224.
PR	26-JUL-1999;	99US-0145276.
PR	27-JUL-1999;	99US-0145913.
PR	27-JUL-1999;	99US-0145918.
PR	27-JUL-1999;	99US-0145919.
PR	28-JUL-1999;	99US-0145951.
PR	02-AUG-1999;	99US-0146386.
PR	02-AUG-1999;	99US-0146388.
PR	02-AUG-1999;	99US-0146389.
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PR	04-AUG-1999;	99US-0147302.
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PR	05-AUG-1999;	99US-0147260.
PR	06-AUG-1999;	99US-0147303.
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PR	10-AUG-1999;	99US-0148171.
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PR	13-AUG-1999;	99US-0148565.
PR	13-AUG-1999;	99US-0148684.
PR	16-AUG-1999;	99US-0149368.
PR	17-AUG-1999;	99US-0149175.
PR	18-AUG-1999;	99US-0149426.
PR	20-AUG-1999;	99US-0149722.
PR	20-AUG-1999;	99US-0149723.
PR	20-AUG-1999;	99US-0149929.
PR	23-AUG-1999;	99US-0149902.
PR	23-AUG-1999;	99US-0149930.
PR	25-AUG-1999;	99US-0150566.
PR	26-AUG-1999;	99US-0150884.
PR	27-AUG-1999;	99US-0151065.
PR	27-AUG-1999;	99US-0151066.
PR	27-AUG-1999;	99US-0151080.
PR	30-AUG-1999;	99US-0151303.
PR	31-AUG-1999;	99US-0151438.
PR	01-SEP-1999;	99US-0151930.
PR	07-SEP-1999;	99US-0152363.
PR	10-SEP-1999;	99US-0153070.
PR	13-SEP-1999;	99US-0153758.
PR	15-SEP-1999;	99US-0154018.
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PR	20-SEP-1999;	99US-0154779.
PR	22-SEP-1999;	99US-0155139.
PR	23-SEP-1999;	99US-0155486.
PR	24-SEP-1999;	99US-0155659.
PR	28-SEP-1999;	99US-0156458.
PR	28-SEP-1999;	99US-0156596.
PR	04-OCT-1999;	99US-0157117.
PR	05-OCT-1999;	99US-0157753.
PR	06-OCT-1999;	99US-0157865.
PR	07-OCT-1999;	99US-0158029.
PR	08-OCT-1999;	99US-0158232.
PR	12-OCT-1999;	99US-0158369.
PR	13-OCT-1999;	99US-0159293.
PR	13-OCT-1999;	99US-0159294.
PR	13-OCT-1999;	99US-0159295.
PR	14-OCT-1999;	99US-0159329.
PR	14-OCT-1999;	99US-0159330.
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PR	14-OCT-1999;	99US-0159637.
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PR	21-OCT-1999;	99US-0160741.
PR	21-OCT-1999;	99US-0160767.
PR	21-OCT-1999;	99US-0160768.
PR	21-OCT-1999;	99US-0160770.
PR	21-OCT-1999;	99US-0160814.
PR	21-OCT-1999;	99US-0160815.
PR	22-OCT-1999;	99US-0160980.
PR	22-OCT-1999;	99US-0160981.
PR	22-OCT-1999;	99US-0160989.
PR	25-OCT-1999;	99US-0161404.
PR	25-OCT-1999;	99US-0161405.
PR	25-OCT-1999;	99US-0161406.
PR	26-OCT-1999;	99US-0161359.
PR	26-OCT-1999;	99US-0161360.
PR	26-OCT-1999;	99US-0161361.
PR	28-OCT-1999;	99US-0161920.
PR	28-OCT-1999;	99US-0161992.
PR	28-OCT-1999;	99US-0161993.
PR	29-OCT-1999;	99US-0162142.
Query Match 96.8%; Score 2671; DB 21; Length 518;		
Best Local Similarity 100.0%; Pred. No. 3.5e-248;		
Matches 518; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	15	MMNEEDGCGMDELLAVLGKVRSSSEADYVAQKLEQLEVMNSVQEDDLSQLATETVHY 74
Db	1	mmneeedgngmdellavlgkvrsssemadvqkleglevmmsnvqeddisqlatetvhy 60
Qy	75	NPAELYTWLDSMLTDLPSPSSNAEYDLKAI PGDAILNFAIDSSASSNOGGGDTYTNK 134
Db	61	npaelytwldsmldclnppssnaeydydkaipgdailnqfaidsassnqgggdytnk 120
Qy	135	RLKCSNGVETTATTAESTRHRVLDVDSQENGVRVLHALLACAEAVQKENTVAEALVKQI 194
Db	121	rlkcsngvettataestrrhvlvdsqengvrivhallacaeavqkentalvaealvki 180
Qy	195	GFLAVSQIGAMRKVATYFAEALARRIYRLSPSQSPIDHSLSDTLQMHFYETCPYLKTAHF 254
Db	181	gflavsqigamrkvatyfaealarriylrspsqspidhslsdtlqmhfyetcpylktahf 240
Qy	255	TANQAIIEAFOGKKRVHVDFSMGSLQWPALMOALALRPGGPPVFRITGTIGPPAPDNFD 314
Db	241	tanqaiieafgqkkrvhvdfsmgslqwpalmqalalrpggppvfrlgtigppapdnfd 300
Qy	315	YLHEVGCKLAHLAEIAHVEFEYRGFVANTLADLDASMLELRPSETESYAVNSVFELHKL 374
Db	301	ylhevqcklahlaeahvefeyrgfvantladldasmllelrpseiesvavnsvfelhkl 360
Qy	375	GRGAIDKVLGVVNOIKPEITFTVVEQSNHNSPIFLDRFTESLHYSTLFDLSLEGVPSGQ 434

PA (ADAM/) ADAM L.
PA (RIEC/) RIECHMANN J L.
PA (YUGG/) YU G.
PA (SAMA/) SAMAHA R.
XX
XX
PI Jiang C, Heard J, Pineda O, Pilgrim M, Adam L, Riechmann JL;
PI Yu G, Samaha R;
XX
XX WPI: 2001-335997/35.
DR N-PSDB; AAD06661.
XX
XX Nucleic acids encoding plant transcription factor polypeptides, useful
PT for altering the sugar sensing characteristics of plants and increasing
PT yield, e.g. corn, potato and cotton plants -
XX
XX Claim 4; Page 115-117; 151pp; English.
XX
XX The patent relates to polynucleotides encoding 35 plant transcription
CC factors which may be used to modify phenotype associated with a plant's
CC sugar sensing characteristics and increasing yield when their expression
CC level is altered. Sugars are central regulatory molecules that control
CC aspects of physiology, metabolism and development. Therefore the cDNAs
CC and proteins of the invention are useful for modifying the growth and
CC germination rates of plants, photosynthesis, glyoxylate metabolism,
CC respiration, starch and sucrose synthesis and degradation, pathogen
CC response, wounding response, cell cycle regulation, pigmentation,
CC flowering and senescence of plants and for modifying sink-source
CC relationships in seeds, tubers, roots, and other storage organs leading
CC to an increase in yield. The transcription factor polynucleotides and
CC polypeptides may be used to alter the structure and developmental
CC characteristics of plants such as soybean, wheat, corn, potato, cotton,
CC rice, oilseed, sunflower, alfalfa, sugarcane, turf, banana, blackberry,
CC blueberry, strawberry, raspberry, cantaloupe, carrot, cauliflower,
CC coffee, cucumber, eggplant, grapes, honey dew, lettuce, mango, melon,
CC onion, papaya, peas, peppers, pineapple, spinach, squash, sweet corn,
CC tobacco, tomato, watermelon, rosaceous fruits and/or vegetable brassicas.
CC The present sequence is a homolog of Arabidopsis thaliana transcription
CC factor.
XX
XX Sequence 587 AA;
SQ

Query Match 79.48; Score 2189.5; DB 22; Length 587;
Best Local Similarity 74.5%; Pred. No. 1e-201;
Matches 441; Conservative 39; Mismatches 43; Indels 69; Gaps 9;
1 MKRDHHH-----HH-----QDKKTMNNEEDDNGCM-DELLAVLGKVRSSMA 43
1 mkrdhqqfggrlshgtsstssssiskmmvmkkkeedgggmddellavlgkvrssma 60
44 DVAOKLEQVYMSNVQEDLSQATERVHYNPAELYTWLDSMLTDLNPP-----SSN--- 96
61 evaikleqtmmsnvqedgishlatdvtvypelsylswldnmiselpnpplpassngld 120
97 -----AEYDLKATPGDAILNQFAIDSSASSNQGGDYYTNKRLK-CSN-- 140
121 pvlpspeicgfpasdydlkvipgnalyqfpaidssssn-----nqnkrkscspsd 172
141 -----GWV-----ETTATAESTRHVVLVDSQENGVRVHALLACAEAV 179
173 smvtststgtgigvgigtvttttttaaastrsvilvdsqengvrivhalmacaeai 232
180 QKENITVAELVKQIGFVAVSQIGAMRKVATYFAELARRIYRLSPSQSPIDHSLSTFLQ 239
233 qgnnltaealvkqigclavsqagmrkvatyfaealarriyrilspqngidhclsdltq 292
240 MHEVETCPYLKFAHTANQALTEAFOCKRVHVHIDFSMSQGLQWPMALQALRPGPPV 299
293 mhfetcpylkfahntanqalaeafegkrvhvldfsmqgqlgwpmalqalalregppt 352
300 FRLGIGPPAPPDFNDYHEVQCKLAHLAEAIHVEFFYRGVFAVNTLADLDSMLRLRSEI 359
353 frlgiappapdnshlhveqcklaqlaeaihvefyrgfvansladdlasmleirpsdt 412

Qy 360 ESVAVSVFELHKLGRPGAIKVLGVVYVQIKPEITVVEQSNHNSPIFLDRFTESLHY 419
Db 413 eavavsvfclhklgrpggiekvlgvvkqkpviftvveqeshnpgvfldrfteslhy 472
Qy 420 YSTLFDLSLEGVPSQDKVMSEVYLKQICNVVACDGPDRVERHETLSQWRNRFSGSAGFAA 479
Db 473 ystlfdlslegvpsqdkvmsevykqicnlvacegpdvrverhetlsqwnrfsgsglap 532
Qy 480 AHIGSNAFKQASMLLALFNGEGYRVESDGLMLGWHTRPLIATSAWKLTST 531
Db 533 ahlgnsafkqasmllalfngsggyrvveesngclmlgwhtrplittsawklst 584

RESULT 9
AAE01892
ID - AAE01892 standard; Protein; 587 AA.
XX
XX AAE01892;
XX AC
XX DT 31-JUL-2001 (first entry)
XX DE Arabidopsis thaliana transcription factor, G307.
XX KW Transcription factor; biochemical characteristic; controlling element;
KW structural characteristic; developmental characteristic; gene therapy;
KW agricultural biotechnology; plant trait modification.
XX OS Arabidopsis thaliana.
XX FH Key Location/Qualifiers
FT Domain 323..339
FT /label= Conserved_domain
XX WO200136597-A1.
XX 25-MAY-2001.
XX
XX 14-NOV-2000; 2000WO-US31344.
XX
XX 17-NOV-1999; 99US-0166228.
XX 17-APR-2000; 2000US-0197899.
XX 22-AUG-2000; 2000US-0227439.
XX (MEND-) MENDEL BIOTECHNOLOGY INC.
PA (CREE/) CREELMAN R.
PA (YUGG/) YU G.
PA (ADAM/) ADAM L.
PA (RIEC/) RIECHMANN J L.
PA (HEAR/) HEARD J.
PA (SAMA/) SAMAHA R.
PA (PILG/) PILGRIM M.
PA (PINE/) PINEDA O.
PA (JIANG/) JIANG C.
XX Creelman R, Yu G, Adam L, Riechmann JL, Heard J, Samaha R;
PI Pilgrim M, Pineda O, Jiang C;
XX
XX WPI: 2001-335999/35.
DR N-PSDB; AAD05776.
XX
XX Nucleic acids encoding plant transcription factor polypeptides, useful
PT for altering the biochemical characteristics of plants e.g. corn,
PT potato and cotton plants -
XX
XX Claim 4; Page 68-70; 127pp; English.
XX The present sequence is Arabidopsis thaliana transcription factor,
CC G307. The transcription factor is used for altering a plant's
CC biochemical characteristics. The transcription factor may be used to
CC alter the structure and developmental characteristics of plants such as
CC soybean, wheat, corn, potato, cotton, rice, oilseed rape, sunflower,
CC alfalfa, sugar cane, turf, banana, blackberry, blueberry, strawberry,

CC raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber, eggplant,
CC grapes, honey dew, lettuce, mango, melon, onion, papaya, peas, peppers,
CC pineapple, spinach, squash, sweet corn, tobacco, tomato, watermelon,
CC rosaceous fruits and/or vegetable brassicas. Transcription factors are
CC key controlling elements of biological pathways and altering expression
CC levels of 1 or more transcription factors can change entire biological
CC pathways in an organism. Therefore manipulating transcription factor
CC levels in plants offers great potential in agricultural biotechnology
CC for modifying a plant's traits. Transcription factor cDNA is useful in
CC gene therapy.
XX
SQ Sequence 587 AA;

Query Match 79.4%; Score 2189.5; DB 22; Length 587;
Best Local Similarity 74.5%; Pred. No. 1e-201;
Matches 441; Conservative 39; Mismatches 43; Indels 69; Gaps 9;
Qy 1 MKRDHHH-----HH-----QDKKTMNNEEDGNGM-DELLAVLGKVRSEMA 43
Db 1 mkrdhhgfgqrlshgtsrssssssiskdkmmmvkkeeoggumdelldavlgkvrsema 60
Qy 44 DVAQKLEQLEVMNSVQDDLSQLATENVHYNPAELYTWLDSMLTDLNPP-----SSN-- 96
Db 61 evaqlkeletcmnsvqdgshlatdvtvynpselyswldnmiselnpplpassngld 120
Qy 97 -----AEYDLKAIPGDAILNQFAIDSASSNSQGGGDTYTNKRKL-CSN-- 140
Db 121 pvlpspeicgfpasdydlkvpngaiyqfpaidsssn-----nqnrkksesp 172
Qy 141 -----GWV-----ETTATAESTRHVVLVDSQENGVRVHALLACAEAV 179
Db 173 smvtstgtgigvgigtvtvttttttaaaestrsvilvdsqengvrlvhalmacaeai 232
Qy 180 QKENLTVAEALVKOIGFLAVSQIGAMRKVATYFAEALARRIYRLSPQSQSDHSLSDTLQ 239
Db 233 qqnultiaevalvkgiclawsqagamkvatyfaealarriyrlspqngidhclsdltq 292
Qy 240 MHFYETCPYLKFAHTANOAILAEAFQGGKRVHVIDFSMSQGLQWLPALMQALALRPGGPV 299
Db 293 mhfyetcpylkfahntanqailaeafegkkrvhvidfsmqglqwpalmqalalreggpt 352
Qy 300 FRLTGIGPPAPDNFDYLHEVGCKLAHLAEATHVEFYRGFVANTLADLDASMLRLRSEI 359
Db 353 frltgigppapdnfdylhevgcklaqlaeathvefyrgfvansladldasmlrlrpsdt 412
Qy 360 ESVAVNSVFELHKLGRPGADKVLGVVNOIKPEIFTVVEQESNHNPIFLDRFTESLHY 419
Db 413 eavavnsvfelhklgrpggiekvlgvvkqikpviftvveqeshnpgvflidrfteslhy 472
Qy 420 YSTLFDLSLEGVPSGQDKVMSEVYLGKQICNVVACDGPDRVERHETLSQWRNRFSGAGFAA 479
Db 473 ystlfdlslegvpsgdkvmsevyigkqicnvacegpdvrherhetlsqwnrfsgslap 532
Qy 480 AHIGSNFAKQSMALLAFNGEGYRVESDCGLMGLWHTRPLIATSAWKLT 531
Db 533 ahlgsnafkqasmllsfnsggyrveesngclmglwhtrplittsawklst 584

RESULT 10
AAB31883
ID AAB31883 standard; Protein: 572 AA.
XX
AC AAB31883;
XX
DT 15-MAY-2001 (first entry)
XX
DE Amino acid sequence of a wildtype GRAS protein.
XX
KW GRAS protein; BZH gene; transcription factor; gibberellin; morphogenesis;
KW plant development; dwarf plant; crucifer.
XX
OS Brassica napus.

XX WO200109356-A1.
XX
XX
PD 08-FEB-2001.
XX
PF 02-AUG-2000; 2000WO-FR02216.
XX
PR 02-AUG-1999; 99FR-0010023.
XX
XX (INRG) INRA INST NAT RECH AGRONOMIQUE.
XX
PI Renard M, Delourme R, Barret P, Brunel D, Froger N, Tanguy X;
XX
DR WPI; 2001-182964/18.
DR N-PSDB; AAF25480.
XX
XX New mutant nucleic acid encoding modified GRAS family protein, used to
PT produce dwarf transgenic plants -
XX
XX Example 1; Page 16-17; 28pp; French.
XX
CC The present sequence represents a wild type plant protein of the GRAS
CC family. The specification describes a mutant allele of the BZH gene,
CC which contains a G1695A mutation resulting in the mutation E546K in the
CC protein. GRAS proteins are transcription factors implicated in
CC regulation of the response to gibberellins and thus in control of
CC morphogenesis and plant development. The mutant GRAS protein is
CC used to produce dwarf plants, specifically crucifers. Dwarf plants may
CC be sown earlier (increasing nitrate accumulation without risking
CC excessive stem growth during winter), and have better resistance to
CC cold and lodging. They are also easier to harvest and allow for better
CC monitoring of the crop.
XX
SQ Sequence 572 AA;

Query Match 76.7%; Score 2114.5; DB 22; Length 572;
Best Local Similarity 73.6%; Pred. No. 1.6e-194;
Matches 430; Conservative 34; Mismatches 51; Indels 69; Gaps 9;
Qy 1 MKRDHHH-----HHQDK-----KTMNNEEDGNGMDELLAVLGKVRSE 41
Db 1 mkrdhhgfgqnghtsiagstspavfgkdkmmvkeeod-----dellylgkvrse 56
Qy 42 MADVAQKLEQLEVMNSVQDDLSQLATENVHYNPAELYTWLDSMLTDLNPPSS----- 95
Db 57 maevalkleqletmngnagdglahtatdvtvynpaeelyswldnmiselnpptaatsna 116
Qy 96 -NAEY-----DLKAIPGDAIL--NOFATDSASSNSQGGGDTYTNKRKLKCS 139
Db 117 lnpelnmnnnsfftggdlkaipgnavcrrtsngfafavdss-----nkrklps 165
Qy 140 N-----GVVETT-TATAESTRHVVLVDSQENGVRVHALLACAEAVKENTLV 186
Db 166 sspdsmtvpspagvigtvtvttestcrpildvsqngvrlvhalmacaeavssnlti 225
Qy 187 AEALVKOIGFLAVSQIGAMRKVATYFAEALARRIYRLSPQSQSDHSLSDTLQMHFYETC 246
Db 226 aealvkqigflavsqagamkvatyfaealarriyrlspqtdqidsdltqmhfyet 285
Qy 247 PYLKFAHTANOAILAEAFQGGKRVHVIDFSMSQGLQWLPALMQALALRPGGPVFLRTGIG 306
Db 286 pylkfahntanqailaeafegkkrvhvidfsmqglqwpalmqalalreggppsfrltgig 345
Qy 307 PPAPDNFDYLHEVGCKLAHLAEATHVEFYRGFVANTLADLDASMLRLRSEISETSVAVNS 366
Db 346 ppaadnsdhlhevgcklaqlaeathvefyrgfvansladldasmlrlrsetseavavns 405
Qy 367 VFELHKLGRPGADKVLGVVNOIKPEIFTVVEQESNHNPIFLDRFTESLHYSTLFD 426
Db 406 vfelhklgrtggiekvlgvvkqikpviftvveqeshnpgvflidrfteslhyystlfd 465
Qy 427 LEGVPSGQDKVMSEVYLGKQICNVVACDGPDRVERHETLSQWRNRFSGAGFAAAHIGSNA 486

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Db 466 legapssqdkvmsevyigkqicnlivacegpdvrhetlsqwnrfsgsfapahlgna 525
QY 487 FKOASMLLALFNGGEGYRVEESDGLMLGWHTRLIATSAWKL 530
Db 526 fkgastilalnggegyrveennngclmshwtrplittsawkl 569

RESULT 11
AAB31884
ID AAB31884 standard; Protein: 572 AA.
XX
AC AAB31884;
XX
DT 15-MAY-2001 (first entry)
XX
DE Amino acid sequence of a mutant GRAS protein.
XX
KW GRAS protein; BZH gene; transcription factor; gibberellin; morphogenesis;
KW plant development; dwarf plant; crucifer.
XX
OS Brassica napus.
XX
PN WO200109356-A1.
XX
PD 08-FEB-2001.
XX
PF 02-AUG-2000; 2000WO-FR02216.
XX
PR 02-AUG-1999; 99FR-0010023.
XX
PA (INRG ) INRA INST NAT RECH AGRONOMIQUE.
XX
PI Renard M, Delourme R, Barret P, Brunel D, Froger N, Tanguy X;
XX
DR WPI; 2001-182964/18.
DR N-PSDB; AAF25481.
XX
PT New mutant nucleic acid encoding modified GRAS family protein, used to
PT produce dwarf transgenic plants
PS Claim 4; Page 20-22; 28pp; French.
XX
CC The present sequence represents a mutant plant protein of the GRAS
CC family. The mutant allele of the BZH gene contains a G1695A mutation
CC resulting in the mutation E546K in the protein. GRAS proteins are
CC transcription factors implicated in regulation of the response to
CC gibberellins and thus in control of morphogenesis and plant development.
CC The mutant GRAS protein is used to produce dwarf plants, specifically
CC crucifers. Dwarf plants may be sown earlier (increasing nitrate
CC accumulation without risking excessive stem growth during winter), and
CC have better resistance to cold and lodging. They are also easier to
CC harvest and allow for better monitoring of the crop.
XX
SQ Sequence 572 AA;

```

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Query Match 76.5%; Score 2110.5; DB 22; Length 572;
Best Local Similarity 73.5%; Pred. No. 3.9e-194;
Matches 429; Conservative 35; Mismatches 51; Indels 69; Gaps 9;

QY 1 MKRDHHH-----HHQDK-----KTMWNEEDGNGMDELLAVLGKVRSE 41
Db 1 mkrdlhgfqgnhgtstagsstspavfgdkmmmvkeed-----dellgvlgykvrse 56
QY 42 MADVAQKLEQLEVMWNVQEDDLSQLATETVHYNPAELYTWLDSMLTDLNPPSS----- 95
Db 57 maevallkqietmmnaqdegahlatdtvhympaelyswidmnlteihppaatgsna 116
QY 96 -NAEY-----DLKAIPGDAIL---NQFAIDSASSNQGGGDTYTNKRLKCS 139
Db 117 lnpeinnnnnsftfgdllaipgnavcrrsnqfafavdsss-----nkrlikps 165

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QY 140 N-----GVVETT-TATAESTHRVVLVDSEQNGVRLVHALLACAEAVOKENLTV 186
Db 166 sspdsmtspspagvigtvtvtvtestrplilvdsqngvrlvhalmaeavqssnltl 225
QY 187 AEALVKOIGFLAVSOICAMRKVATYFAEALARRIYRLSPSQSPIDHSLSDTLQWHFYETC 246
Db 226 aealvkqigflavsqagmrkvatyfaealarriyrlspptqgidhslsdltlqmhfyetc 285
QY 247 PYLKFAHFTANOAILLEAFQGGKRVHVHIDFSMSOGLQWPAALMOALALRPGLFRLTGIG 306
Db 286 pylkfahftanqaileafegkkrvhvdfsmmqglqwpalmqalaleggppsflltgig 345
QY 307 PPAPDNFDYLYHEVGCKLAHLAEAIHVEFEYRGFVANTLADLDASMLERSEIESVAVNS 366
Db 346 ppaadnsdhlhevqcklaqlaeaihvefeyrgfvansladldasmlelrpseteavavns 405
QY 367 VFELHKLGRGAIKDKVLGVVNOIKPEFTVVEQESNHNPSIFLDRFTESLHYSTLFD 426
Db 406 vfelhklgrtgglekvfgvkvkqikpvlftveqesnhngpvfldrfteshyystlfd 465
QY 427 LEGVPSGQDKVMSEVYLGKQICNVVACDGPDRVERHETLSQWRNRFSGAGFAAAHIGSNA 486
Db 466 legapssqdkvmsevyigkqicnlivacegpdvrhetlsqwnrfsgsfapahlgna 525
QY 487 FKOASMLLALFNGGEGYRVEESDGLMLGWHTRLIATSAWKL 530
Db 526 fkgastilalnggegyrveennngclmshwtrplittsawkl 569

RESULT 12
AAB28574
ID AAB28574 standard; Protein: 587 AA.
XX
AC AAB28574;
XX
DT 09-FEB-2001 (first entry)
XX
DE Arabidopsis SCLa8.
XX
KW Scarecrow gene; SCR gene; plant; regulatory gene; SCARECROW-like; SCL;
KW transgenic plant; cell division; molecular marker; herbicide resistance;
KW salt resistance; pathogen resistance; insect resistance.
XX
OS Arabidopsis thaliana.
XX
PN WO2000053723-A2.
PD 14-SEP-2000.
XX
PF 07-MAR-2000; 2000WO-US05875.
XX
PR 10-MAR-1999; 99US-0265585.
XX
PA (UUNY ) UNIV NEW YORK STATE.
XX
PI Benfey PN, Di Laurenzio L, Wysocka-Diller J, Malamy JE, Pysh L;
PI Helariutta Y, Bruce W, Lim J;
DR WPI; 2000-594315/56.
DR N-PSDB; AAC65291.
XX
SC Scarecrow gene useful for producing transgenic plants expressing genes
PT whose product increases starch, lignin or cellulose biosynthesis and
PT confers herbicide, pathogen or insect resistance
XX
PS Claim 14; Fig 13; 200pp; English.
XX
CC The present sequence is given in a specification relating to the
CC structure and function of a regulatory gene, SCARECROW (SCR).
CC SCARECROW-like (SCL) genes encoding proteins containing an amino acid
CC sequence similar to the sequence of MOTIF III (WHIR) of Arabidopsis SCR
CC protein are disclosed. SCR and SCL genes are useful for producing
CC transgenic plants whose cell division is modified and root and/or stem

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development and gravitropism of stem or hypocotyl is altered. Cell division is increased or decreased in roots resulting in thicker or thinner root development. The transgenic plants are useful for expressing a gene of interest encoding a gene product that confers herbicide, salt, pathogen or insect resistance in root or embryos and genes encoding starch, lignin or cellulose biosynthesis in shoots. The SCR gene also confers less susceptibility to lodging in the transgenic plants than a wild-type plant. SCR gene sequences are also useful as molecular markers for a quantitative trait e.g. root or gravitropism trait in molecular breeding of crop plants.

Sequence 587 AA;

Query Match	74.7%;	Score 2059.5;	DB 21;	Length 587;
Best Local Similarity	70.8%;	Pred. No. 3.3e-189;		
Matches 419; Conservative	40;	Mismatches 64;	Indels 69;	Gaps 9;

QY	1	MKRDHHH-----HH-----ODKTTMMNEEDDNGM-DELLAVLGKVKRSSEMA	43
Db	1	mkrdhhqfgrlshnhtstssssssiskdkmmvkkkeedggngmdellavlgkvrssma	60
QY	44	DVAQKLEQLEVMKSNVOEDDLSQATETVHYNPAELYTWLDSMLTDLNPP-----SSN----	96
Db	61	evalkietlmtmsnagdeglshlactdaahynpselyswldmlelnpplpasngld	120
QY	97	-----AEYDLKAIPGDALINQFAIDSASSSSOGGGDTYTTNKRKL-CSN--	140
Db	121	pwlpseicgfpxsdylkvpixnalypqaldssssn-----nqqrkksccspd	172
QY	141	-----GVV-----EPTTATAESTRHVLVDISOENGVRVLHALLACAFAV	179
Db	173	smvtststgtqggvgtvtvtvttttttaaaestsvilvdsgengvrihvhalmacaeai	232
QY	180	QKENLTVAEALYKQIGFLAVSQIGAMRKVATYFAEALARRIYRLSPSQSPIDHSLSDTLQ	239
Db	233	qgnnlclaealvkqlgclavsgagmrkvatyaefaalariyrlspqqnqhdcsdltlq	292
QY	240	MHFEYETCPYLKFAHFTANQAILEAFQGGKRVHVDFDSMSQGLQWPAIMOALALRPGGPV	299
Db	293	mhyetcpylkfhaitqancalaeafegkrvhvdfsmnqglqwpalmcalalreggppt	352
QY	300	FRUTGTGPAPDNFDYLHEVGGKLAHLAEAHVPEYRGFVANTLADLDASMLELRPSEI	359
Db	353	frittgppapdnshlhevvgcklaqlaeaihvefyrgfvansladldasmllelrpsdt	412
QY	360	ESVAVNSVFLHKLGLRGPDAIDKVLGVVNOIKPEIFTVVQESNNHSPFLDRFTESLHY	419
Db	413	eavavnsvflhklglrxgglkvivgkdtgdfhwxwrqepnhnpgpflgdxceslhy	472
QY	420	YSTLPDLSLEGVPSGDBKVMSEVVLGKQICNVVACDGFDRVERHETLSQWRNRFFGSAGFAA	479
Db	473	ystxfdslegxpsqdklmsexylgxqicnlvacegpdvrhethltsqwnrfgsgslap	532
QY	480	AHTGSNAFQOASMLLALFNFGGEGYRVVEESDGGCLMLGNWHTPLIATSAWKLST	531
Db	533	ahlgnsafkqasmlslsvfqqggyrveesngclmlqwhtrplittsawklst	584

RESULT 13

RESOLU
AAY02541

ID AAY02541 standard; Protein; 630 AA.

AA
AC AAY02541:

16-JUL-1999 (first entry)

DE Protein encoded by maize 1al genomic clone sequence.

Rht gene; homologue; *Triticum aestivum*; wheat; growth inhibition;
 KW antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;
 KW paclobutrazol; maize.

XX
XXOS
Zea mays.

OS
XX
PN

25 - FEB - 1999.

XX 07-AUG-1998:

XX
PR 13-AUG-1997. 97GB-0017192XX
PA (PLAN-) PLANT PROSCIENCE LTDXX
PI
Harberd NP. Peng J. Richards DE:XX
DR WPT: 1999-181040/15

DK WFI; I999-I8I040/
DR N-PSDB: AAX36280.

AA New Triticum Aestivum polynucleotides - encode a polypeptide which
PT provides inhibition of the growth of plants, which inhibition is
PT antagonised by gibberellin, used to confer a dwarf phenotype
PT

PS Disclosure: Fig 9b; 88pp; English;

The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in *Triticum Aestivum*, inhibit growth of the plant. This growth inhibition is antagonised by gibberellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin-insensitive. Taller plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin biosynthesis, such as paclobutrazol e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds dwarf but let crop plants grow tall. The present sequence is encoded by the maize 1a1 genomic clone sequence.

AA	Sequence	630 AA;
SQ		

Query Match	58.18;	Score 1602.5;	DB 20;	Length 630;
Best Local Similarity	54.0%;	Pred. NO. 3.8e-145;		

0y 1 MKRDRHHHHHOD-----KKTMM-----NEEDDNGNGMDEL.I.AVI.GYKVRSSSEM 42

1 mkre---vdaaasaaamasskdmmmaaaacaeceeed---vde|aalaykvrssdm 53

07 43 ADVAOKI EOI EYMM-----SNVOEDD--I SOI ATETVHYNDPAEY VTWI DSMI TDI NBP Q3

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QY ZI4 EALARRIYRL--SPSQSPIDHSLSDITLQMHFYETCPYLKFAHF"ANQAILEAFQGKRRVH 277

Bb 289 eaIarvyrirppdssIIdaaIadIIhantIescpyIkrantItanqalIearIagcrrvH 34

QY 272 VIDFMSQGLQWPALMQALALRPGGPPVFRLTGIGPPAPDNFDYLHEVGCKLAHLAEAIH 33

Db 349 vdfgikgmgwpa11qalalrpggppsfrltvgppqpdetdalqqvgwklagfahtir 40

QY 332 VEFYRFGVANTLADLADSMLELR-----PSEIESVAVNSVNFELHKLGRPGAIKRVLGV 387
Db 409 vdfyrgivaatlaladlqfmglddtddepeviavnsvfhelrlaagalekvlgvt 468
QY 388 NOIKPEIFTVVVOESNHNPSIFLDRFTESLHYSTLPSLEGVPSGQ----- 434
Db 469 ravprlvvveqeanhnsgrtldfreslhysscmfsllegagsgsgtdaspaagg 528
QY 435 -DKVMSEVYLKQICNVVACDGPDRVERHETLSQWRNRFSGAGFAAAHIGSNAPKQASML 493
Db 529 lqdvmsvylgrqicnvvacageaeterhetlgqwrslggsgfapvhlgsnaykqastl 588
QY 494 LALFNGGCGYRVEESDGLMLGWHTRPLIATSAWKL 530
Db 589 lalfaggdgyrveekdglctlgwhtrpliataswrv 625

RESULT 14
AA02540
ID AA02540 standard; Protein: 623 AA.
AC AA02540;
DT 16-JUL-1999 (first entry)
XX Protein encoded by wheat Rht clone 5a1 genomic sequence.
DE Rht gene; homologue; Triticum aestivum; wheat; growth inhibition;
KW antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;
KW paclobutrazol.
XX Triticum aestivum.
XX WO9909174-A1.
XX 25-FEB-1999.
XX 07-AUG-1998; 98WO-GB02383.
XX 13-AUG-1997; 97GB-0017192.
XX (PLAN-) PLANT BIOSCIENCE LTD.
PI Harberd NP, Peng J, Richards DE;
DR WPI; 1999-181040/15.
XX N-PSDB; AAX36279.

PT New Triticum Aestivum polynucleotides - encode a polypeptide which
PT provides inhibition of the growth of plants, which inhibition is
PT antagonised by gibberellin, used to confer a dwarf phenotype
XX Disclosure; Fig 8b; 88pp; English.
XX The specification describes polypeptides encoded by the Rht gene (and
CC its homologues) that, when expressed in Triticum Aestivum, inhibit
CC growth of the plant. This growth inhibition is antagonised by
CC gibberellin. The products can be used to provide Rht expression in
CC plants, conferring a dwarf phenotype on a plant which is correctable
CC by treatment with gibberellin. In addition, the products can be
CC used to produce Rht mutant plants which are dwarfed compared with
CC wild-type, the dwarfing being gibberellin-insensitive. Taller plants
CC may be made by knocking out Rht or the relevant homologous gene in
CC the plant of interest. Plants may be made which are resistant to
CC compounds which inhibit gibberellin biosynthesis, such as paclobutrazol,
CC e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds
CC dwarf but let crop plants grow tall. The present sequence is encoded by
CC the wheat Rht clone 5a1 genomic sequence.

XX Sequence 623 AA;

Query Match 57.88; Score 1594; DB 20; Length 623;

Best Local Similarity 54.3%; Pred. No. 2.5e-144;
Matches 332; Conservative 71; Mismatches 106; Indels 102; Gaps 11;
QY 11 DKKTMMNEEDDGGNGMDLLAVLGKVKRSSEMDVAAKLEQLEVM-----SNVQEDD- 63
Db 22 edkmvsaagaageevdellaalgkykrasmdadvakleqlamangmgvgagaapdds 81
QY 64 -LSLATETVHYNPAELYTWLDSMLTDLNPP----- 93
Db 82 fathlatvtvnyptdlsswvesmlseinaappplppapqinaststvtgsggydfldpp 141
QY 94 ---SSNAEYDLKAP-----CDAIL-----NQFAIDSASSNQGGGDT 129
Db 142 svdsssiyalrppspagatapadlsadvrdpkrmttggstsssssssggg--- 198
QY 130 YTNKRLKCSNGVVE-----TTTATAESTRHWLVVDSENGVRLVHALLACAEAVOKENL 184
Db 199 -----arssvveaappvaaaanataplvvvvdtgeagirlvhallacaeavqenl 250
QY 185 TVAPALVKQIGFLAVSQIGAMRKVATYFAEALARIYRL--SPSQSPIDHSLDLOMHF 242
Db 251 saaealvkipllaasqggamrkvaayfgealarvfrfpqpdssllidaafadilhahf 310
QY 243 YETCPYLKFAHFTANQAILLEAFQKKRVHVIDFSQSLQWLPALMQALALRPGPPVRL 302
Db 311 yescpylkfahftanqailleafagcrrvhvvdgfkqgmwpallqalalrpggppsfri 370
QY 303 TGICPPAPDNFYLHEVGCKLAHLAEATHVEFYRGFVANTLADLDASML----ELRPS- 357
Db 371 tgvpppdpdelalqvgvkwlaqfahrtirvdfqyrglvaatladielpfmpegeedpne 430
QY 358 EIESVAVNSVFEHLKLGKRGCAIDKVLGVNQIKPEIFTVVVEQESNHNPSIFLDRFTESL 417
Db 431 epeviavnsvfemhrlaqpalekvlgtravprlvvvegeanhsgrfldrftesl 490
QY 418 HXYSTLFDLSLES-----VPSGODKVMSEVYLKQICNVVACDGPDRV 459
Db 491 hystcmfslslegsgsggppsevsgaaagtdqvmsevygrqicnvvacageaert 550
QY 460 ERHETLSQWRNRFSGAGFAAAHIGSNAPKQASMLLALFNGGEGYRVEESDGLMLGWHTR 519
Db 551 erhetlgqwrnrlgnagfetvhlgsnaykqastllalfaggdgykveeegcltligwhtr 610
QY 520 PLIATSAWKL 530
Db 611 pliataswrla 621

RESULT 15
AA02539
ID AA02539 standard; Protein: 425 AA.
XX AC AA02539;
XX DT 16-JUL-1999 (first entry)
XX DE Protein encoded by the wheat Rht clone C15-1 cDNA sequence.
XX KW Rht gene; homologue; Triticum aestivum; wheat; growth inhibition;
KW antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;
KW paclobutrazol.
XX OS Triticum aestivum.
XX WO9909174-A1.
XX PN 25-FEB-1999.
XX PD 07-AUG-1998; 98WO-GB02383.
XX PF 13-AUG-1997; 97GB-0017192.
XX PR (PLAN-) PLANT BIOSCIENCE LTD.
PA

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XX Harberd NP, Peng J, Richards DE;
PI WPI: 1999-181040/15.
DR N-PSDB; AAX36278.
XX
XX New Triticum Aestivum polynucleotides - encode a polypeptide which
PT provides inhibition of the growth of plants, which inhibition is
PT antagonised by gibberellin, used to confer a dwarf phenotype
XX
XX Disclosure; Fig 7b; 88pp; English.
XX
XX The specification describes polypeptides encoded by the Rht gene (and
CC its homologues) that, when expressed in Triticum Aestivum, inhibit
CC growth of the plant. This growth inhibition is antagonised by
CC gibberellin. The products can be used to provide Rht expression in
CC plants, conferring a dwarf phenotype on a plant which is correctable
CC by treatment with gibberellin. In addition, the products can be
CC used to produce Rht mutant plants which are dwarfed compared with
CC wild-type, the dwarfing being gibberellin-insensitive. Taller plants
CC may be made by knocking out Rht or the relevant homologous gene in
CC the plant of interest. Plants may be made which are resistant to
CC compounds which inhibit gibberellin biosynthesis, such as paclobutrazol,
CC e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds
CC dwarf but let crop plants grow tall. The present sequence is encoded by
CC the wheat Rht clone C15-1 cDNA sequence.
XX
SQ Sequence 425 AA;
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Query Match 49.9%; Score 1375; DB 20; Length 425;
Best Local Similarity 64.4%; Pred. No. 1.6e-123;
Matches 271; Conservative 46; Mismatches 74; Indels 30; Gaps 5;

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QY 140 NGVVE-----TTATASTRHVLVDSQENGVRVLVHALLACAAEVOKENLTVAEALVKQI 194
Db 3 ssvveaappvaanaanatpalpvvvvtdqagirlvhallacaeavqgenlsaaealvkqi 62

QY 195 GLAVSQIGAMRKVATYFAEALARRIYRL--SPSQSPIDHSLSDTLQMHFYETCPYLKFA 252
Db 63 pllaasggggnrkvaayfgealarvfrfpqpsdlldaafadllhahfyescpylkfa 122

QY 253 HFTANQALIEAFQSKKRVRHVVDIFSMSQGLQWPALMQALALRPGGPPVFRLTGIGPPAPDN 312
Db 123 hftanqaileaafagrrrvhvvdfigkgmqwpallqalalrpggppsfrltgvgppqpd 182

QY 313 FDYLHEVGCKLAHLAEATHVEFYRGFVANTLADLASML---ELRPS-EIESVAVNSV 367
Db 183 tdaigqvgwklaqfahtirvdfqrglvaatiadlepmlqpegeedpneepeviavnsv 242

QY 368 FELHKLGRGAIDKVLGVVNVQIKPEFTVVEQESNNHNSPIFLDRFTESLHYSTFLDLSL 427
Db 243 femhrliaqpgalekvgtvavtrprlvtvvegeanhnsgtfldrfteslhystmfdsl 302

QY 428 EG-----VPSGQDKVMSEYVLCKQICNVVACDGPDRVERHETLSQWR 469
Db 303 eggssgggspvssvsgaaapaagtdqvmsevyigrqicnvvacageaerterhetlqqr 362

QY 470 NRFGSAGFAAAHIGSNAPKQASMLIALFNNGEGYRVESDGCLMLGWHTRELIATSAWKL 529
Db 363 nrlgnagfetvhlgsnaykqastlialfagdgdykveekgccltlgwhtrpliatsawrl 422

QY 530 S 530
Db 423 a 423
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